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REMARKS

The Notice of Non-Compliant Amendment states that the claims filed on April 16, 2004 do not comply with the requirements of 37 C.F.R. § 1.121(c) because claims 28 and 29 are listed as "previously presented" but in fact are "currently amended." In response, Applicants are submitting an Amendment which is substantially similar to the Amendment filed on April 16, 2004, but which has been amended to correct this inadvertent error.

After entry of this Amendment, claims 14, 16-20, 23-29, 31-32 and 35-37 will be pending and under consideration in this application.

Claims 14, 16, 19-20, 23-29 and 31-32 have been amended. Claims 35-41 have been added. Support for the claim amendments and for the new claims can be found throughout the specification. (The specific support for the claim amendments and new claims will be discussed below.) Applicants respectfully submit that none of the claim amendments add new matter to the application.

Claims 1, 3-4, 7-9 and 12-13 have been cancelled without prejudice. Applicants reserve the right to file an application which claims priority to the instant application and contains the subject matter of the cancelled claims.

Indefiniteness Rejections under 35 U.S.C. §112, ¶2

The Examiner has rejected claims 1, 3, 4, 7-9, 12-14, 16-20, 23-29, 31 and 32 under 35 U.S.C. §112, ¶2, as being indefinite due to their recitation of M64347_at. The Examiner states that M64347_at is a GenBank Accession No. and therefore an object which is variable.

Claims 1, 3-4, 7- 9 12 and 13 have been cancelled and, therefore, the rejection with respect to these claims has been obviated.

Applicants respectfully traverse the rejection with respect to claims 14, 16-20, 23-29, 31 and 32, which have been amended to refer to an informative gene comprising certain nucleotides of GenBank Accession No. M64347. Support for this amendment can be found at in the specification which discloses that the Affymetrix "HuGeneFL array" was used, and that M64347_at marker was upregulated. *See* Amendments to the Specification submitted in July 30, 2003, under the heading "Microarray hybridization" and Table 1. As indicated in the Affymetrix

website (Exhibit A), M64347_at refers to a set of probes which detect nucleotides 3336-3720 of GenBank Accession No. M64347.

Applicants submit that reference to a GenBank Accession No. does not render the claims indefinite. A person of ordinary skill in the art would be able to determine the nucleotide sequence of a gene by reference to its GenBank Accession No. Further, while a GenBank Accession No. can be revised, a person of ordinary skill in the art would be to identify any revisions made to a sequence over time. Attached as Exhibit B is print-out from the National Center for Biotechnology Information ("NCBI") website which summarizes their policy with respect to sequences revisions (*see* page 1 of the Exhibit), and states that a person reviewing the records for a particular GenBank Accession No. would be able to determine whether a particular sequence has been revised and would be able to access previous versions of the sequence (*see* page 3 of the Exhibit).

Furthermore, a search of the United States Patent and Trademarks Office ("USPTO") granted patents database reveals that the USPTO has granted patents containing claims which recite sequences by references to their GenBank Accession Nos.[1] Thus, Applicants respectfully request that the Examiner withdraw this rejection.

The Examiner has also rejected claims 12-13, 24-25, 28 and 29 for referring to Table 1 and Tables 2-6. Further, the Examiner states that the reference to the genes in Tables 1-6 by reference to their GenBank Accession Nos. renders the claims indefinite.

Claims 12 and 13 have been cancelled and, therefore, the rejection with respect to these claims has been obviated.

Claims 24-25, 28 and 29 have been amended to replace the reference to the Tables with reference to the GenBank Accession Nos. for the genes disclosed in the Table. Support for this amendment can be found at Tables 1 and 6. Table 1 lists the genes by reference to the probes used to detect the genes disclosed in Table 1, which correlate to the GenBank Accession Nos. for the genes disclosed in the Table 1. Exhibit C provides information obtained from the Affymetrix website which shows such correlation. Note that Exhibit C does not provide the information for all of the probes disclosed in Table 1 since the purpose of the exhibit is to

[1] The query used was: "GenBank Accession Number" or "GenBank Accession No." in claims. This search resulted in 18 hits. Among the relevant hits were: U.S. Patent Nos. 6,667,065, 6,627,193, 6,468,773, and others.

demonstrate that the reference to the probes in Table 1 correlates with the GenBank Accession Nos. of the genes disclosed in Table 1.

Applicants traverse the Examiner's statement that references to GenBank Accession Nos. render the claims indefinite for the reasons discussed above. Accordingly, Applicants respectfully submit that the scope of claims 24-25, 28 and 29 is definite, and request the Examiner to withdraw this rejection.

Applicants note that claims 40 and 41 have been added. Support for the claims can be found throughout the specification, particularly at Tables 1 and 6. Applicants respectfully submit that claims 40 and 41 are definite.

The Examiner has rejected claim 1 as indefinite "for failing to [show the] how the expression profile is correlated with a specific brain tumor type." Further, the Examiner states that "the metes and bounds of two or more informative genes beyond the M64347" is unclear. Claim 1 has been cancelled and, therefore, this rejection has been obviated.

The Examiner has rejected claims 8, 9, 19 and 20 as indefinite because they "lack active method steps, as the recitation of 'utilizing' does not constitute a specific method step."

Claims 8 and 9 have been cancelled and, therefore, the rejection with respect to these claims has been obviated. Applicants respectfully traverse this rejection with respect to claims 19 and 20. Applicants submit that the recitation of "utilizing" in claims 19 and 20 is not intended to be a further method step. Instead the recitation of utilizing provides a further definition of how to determine a gene expression profile. Applicants have amended the claims to improve their form and clarify this point. Accordingly, Applicants respectfully request that the Examiner withdraw this rejection.

The Examiner has rejected claim 14 as indefinite because the use of the term "the sample" lacks antecedent basis. Claim 14 as amended refers to "the brain tumor" rather than "the sample." This amendment renders the rejection moot.

The Examiner has rejected claim 23 as indefinite for its recitation of "survival after treatment" as the predicted treatment outcome. Applicants have amended claim 23 to require the predicted treatment outcome to be a good prognosis of survival after treatment or treatment failure. Support for amended claim 23 can be found at page 9, lines 23-26 of the Substitute Specification. This amendment renders the rejection moot.

The Examiner has rejected claims 26 and 27 as indefinite because of their recitation of: "informative genes", "magnitude", "class distinction", "winning", and "summing the votes", "the sample to be tested", "first class" and "second class". (*See* Office Action, pages 3-4.) More specifically, with respect to claim 26, the Examiner states that "it is unclear how the 'magnitude' of the vote is to be determined because 'depending on the expression level of the gene' does not accurately define the mathematical relationship between the gene expression and the magnitude of the vote" (Office Action, page 3).

In response to the Examiner's rejections of claims 26 and 27, Applicants traverse in part and amend in part. Applicants have amended these claims to improve their form and to more clearly define the claimed invention. Applicants respectfully submit that the amended claims would be considered definite by a person having ordinary skill in the art.

The claims as amended require calculating the weighted vote of each informative gene. According to the specification, "informative genes" refers to "genes whose expression correlates with a particular phenotype." (*See* Substitute Specification, page 8, lines 23-25 and page 9, lines 13-16.) Thus, with respect to claims 26 and 27, an informative gene is one which correlates with treatment outcome.

Further, the claims have been amended to clarify "class distinction", "first class" and "second class". Applicants respectfully submit that based on the information disclosed in the specification and the knowledge in the art, a person of skill in the art at the time the application was filed would be able to calculate the weighted vote for an informative gene, and to sum up the votes to determine a winning class as required by claims 21 and 22. The weighted voting algorithm was well known in the art at the time the application was filed as evidenced by the fact that the specification cites to three references which use this method. *See* Substitute Specification, page 32, lines 27-28 and Amendments to the Specification submitted in July 30, 2003, under the heading "Weighted Voting", citing to: U.S. Application No. 09/544,627 (now issued as U.S. Patent No. 6,647,341), Golub 1999, and Slonim 2000.

Finally, the Examiner states that claims 26 and 27 are vague and indefinite because it is unclear if the level of gene expression used in the computation is a normalized or non-normalized level. Applicants respectfully traverse. Applicants submit that it is irrelevant to the claimed methods, and that a person of skill in the art would know whether the gene expression

level should be normalized or non-normalized in a particular instance. Accordingly, Applicants respectfully request that the Examiner withdraw this rejection.

Enablement Rejections under 35 U.S.C. §112, ¶1

The Examiner has rejected claims 1, 3, 4, 7-9, 12-14, 16-20 and 23-29 for lack of enablement.

Applicants have cancelled claims 1, 3, 4, 7-9, 12 and 13, directed to methods of classifying a brain tumor. Therefore, the Examiner's rejections with respect to these claims have been obviated.

Applicants traverse the Examiner's enablement rejection with respect to claims 14, 16-20 and 23-29, directed to methods of predicting the efficacy of treating a brain tumor, methods for predicting a treatment outcome of a patient with a brain tumor, methods for evaluating drug candidates for their effectiveness in treating a brain tumor or methods for monitoring the efficacy of a brain tumor.

According to the Examiner, "[t]here are no teachings in the specification to correlate a value which is several standard deviations from the mean with a method of predicting the efficacy of a brain tumor. More specifically, the Examiner states that: (1) the specification does not teach whether the expression of M64347 as shown in Figure 3C was obtained from the brain tumor before treatment or after treatment, (2) it is unclear if the lowered expression of M64347 is indicative or predictive of treatment failure or a treatment success as the title of Figure 3C is "Markers of Treatment Failure" but the heading of Table 1 is "Markers Downregulated with Low Risk" and (3) the specification does not define how the C1 or C0 groups were differentiated and does not teach what constitutes a treatment failure or success in terms of disease free survival or length of survival.

As mentioned above, Applicants traverse. First, the specification teaches that expression of M64347 as shown in Figure 3C was obtained from the brain tumor before treatment. *See* Substitute Specification, page 40, line 28 to page 41, line 2.

Second, the specification (Table 1, Table 6 and Figure 3C) shows that the upregulation of M64347 is correlated with a "high risk class" of individuals (*e.g.*, a class of individuals with

poor prognosis for survival after treatment). *See* Substitute Specification, page 9, lines 13-16 stating that "a sample can be classified as belonging to a high risk class (e.g., a class with poor prognosis for survival after treatment) or a low risk class (e.g., a class with good prognosis for survival after treatment)." Thus, the heading of Table 1 – "Markers Upregulated in High Risk, Downregulated in low Risk" – is not inconsistent with the heading of Figure 3C – "Markers of Treatment Failure" – as it appears to be suggested by the Examiner.

Third, the specification describes that in Figure 3 C0 and C1 correspond to two unsupervised SOM-derived clusters, and that Class C1 tumors are notable for their high ribosomal content. *See* Substitute Specification, page 7, lines 2-4. The specification further states that the C0 and C1 groups were not correlated with patient survival. *See* Substitute Specification, page 41, lines 13-17.

Finally, the specification teaches what constitutes treatment failure or success in terms of disease free survival or length of survival. The specification states that they differentiated "patients who are alive following treatment ('survivors') compared to those [patients] who succumbed to their disease ('failures'; minimum follow-up 24 months for surviving patients; overall median 41.5 months)." *See* Substitute Specification page 41, lines 17-21.

The Examiner also states that "[t]here is no guidance for a specific polynucleotide probe and hybridization conditions to be used in the determination of an expression profile for . . . the method of predicting the efficacy of treatment." The Examiner noted there are different isoforms of FGFR3, the gene encoded by M64347, and stated that a probe to this gene could hybridize to any number of the polymorphic gene products or alleles. The Examiner concluded that the "specification provides no teachings as to the exact nature of the probe used for the expression profile, thus it cannot be construed from the specification which polymorphic variants, splice variants or alleles are integral to the claimed invention."

Applicants note that not all of the claims recite the use of a probe and/or require the use of hybridization condition to determine an expression profile. In any case, Applicants respectfully traverse the Examiner's rejection to the extent that certain claims require the use of a specific polynucleotide probe and hybridization conditions.

Contrary to the Examiner's assertion, the specification teaches the exact nature of the probes used to determine the expression profiles for the classification of a brain tumor, or the

method of predicting the efficacy of treatment. The specification states that they used Affymetrix's HuGeneFL array. (*See* Amendments to the Specification submitted in July 30, 2003, under the heading "Microarray hybridization.") Based on this disclosure, a person of skill in the art would have been able to identify the probes present in the array and used in the specification to determine the expression profiles for the method of predicting the efficacy of treating a brain tumor.

More specifically, based on the disclosure, a person skilled in the art would have been able to determine the specific probe used to determine the expression profile of M64347, and the other informative genes disclosed in the specification. The claims have been amended to recite an informative gene comprising nucleotides 3336-3720 of GenBank Accession No. M64347, which are the nucleotide sequences in Affymetrix's HuGeneFL array. *See* Exhibit A (obtained from Affymetrix's website). Thus, Applicants submit that the claims, as amended, are enabled with respect to the probes which can be used to practice the methods of the claimed invention.

Applicants respectfully submit that, in view of the specification, which teaches that the expression profile of an informative gene which hybridizes to nucleotides 3336 to 3720 of GenBank Accession No. M64347 correlates with efficacy of treating a brain tumor, the fact that there are different allelic variants or isoforms of the gene encoded by GenBank Accession No. M64347 is irrelevant.

Applicants respectfully submit that a person of ordinary skill in the art would know what hybridization conditions should be employed to determine the expression profile of the informative genes of the claims. Moreover, the specification teaches the hybridization conditions used in the experiments disclosed in the specification. (*See* Amendments to the Specification submitted in July 30, 2003, under the heading "Microarray hybridization.") Thus, Applicants submit that the claims are enabled with respect to the hybridization conditions useful in practicing the methods of the claimed invention.

With respect to claims 26-29, the Examiner states that "the specification does not define the parameters needed to calculated weighted vote for M64347." Applicants respectfully traverse. As discussed above, based on the information disclosed in the specification, a person of skill in the art would know how to determine weighted vote as recited in the claims without undue experimentation as evidenced by the fact that the specification refers to a patent

application (U.S. Application No. 09/544,627, now issued as U.S. Patent No. 6,647,341) and two papers (Golub 1999 and Slonim 2000) that disclose the use of this weighted voting algorithm before the instant application was filed. (*See* Substitute Specification, page 32, lines 27-28 and Amendments to the Specification submitted in July 30, 2003, under the heading "Weighted Voting.")

The Examiner states that "Applicants arguments regarding the teachings of Golub et al. for methods of determining class and subclass as set forth in U.S. application No. 09/544,627 are unpersuasive" because the instant application could issue before the referenced application. (*See* Office Action, page 7.) Applicants note that the referenced application has now issued as U.S. Patent No. 6,647,341. Applicants have amended the application accordingly.

In view of the arguments presented above, Applicants respectfully request that the Examiner withdraw the enablement rejections.

Obviousness Rejections

The Examiner has rejected claims 31 and 32 under 35 U.S.C. §103(a) as being unpatentable over U.S. Patent No. 6,500,938 ("*Au-Young*") in view of Abbass et al., 1997, *J. Clin. Endocrinol. Metab.*, 82:1160-1166) ("*Abbass*"), or over U.S. Patent No. 6,218,122 ("*Friend*") in view of *Abbass*.

The Examiner alleges that *Au-Young* teaches methods of monitoring the progression of a disease or the efficacy of a treatment comprising detecting an expression profile by means of a micro array. The Examiner alleges that *Friend* teaches methods for detecting changes in a biological state of a subject which are correlated to one or more disease states and methods for monitoring the efficacies of a therapy comprising the determination of an expression profile from said cells in a patient. However, as admitted by the Examiner, neither *Au-Young* nor *Friend* teaches the expression profile of M64347 or the FGFR3 encoded thereby.

The Examiner alleges that *Abbass* teaches "that the expression of the mRNA encoding the secreted form of FGFR3, which would be expressed from the M64347_at gene, is correlated with pituitary adenomas." Further, as admitted by the Examiner, *Abbass* does not teach a correlation between the expression profile of FGFR3 and tumor type, size or aggressiveness. (*See* 12/31/03 Office Action, page 5.)

It is respectfully pointed out to the Examiner that a proper rejection based on 35 U.S.C. §103 that relies on a combination of prior art references requires a teaching, suggestion, or motivation to combine the teachings of the references; a reasonable expectation of success founded in the cited art of producing the claimed invention; and that such proper combination teaches or suggests all elements of the claimed invention. Applicants respectfully traverse the obviousness rejections for failing to meet all of these requirements for the reasons provided below.

Claims 31 and 32, as amended, recite methods for evaluating drug candidates for their effectiveness in treating brain tumors or methods for monitoring the efficacy of a brain tumor treatment, wherein the brain tumor is selected form the group consisting of mellanoblastomas, glioblastomas, rhabdoid tumors, primitive neuroectodermal tumors, and pineoblastomas. Support for this amendment, and for newly added claims 35-39, can be found throughout the specification. *See, e.g.,* Substitute Specification, page 3, lines 1-2.

Applicants respectfully submit that there is no motivation to combine the references cited by the Examiner to reach the invention of amended claims 31 and 32. The Examiner states that "one of ordinary skill in the art would have been motivated to [combine the references] with a reasonable expectation of success by the teachings of Abbass et al. on the unique expression of the secretable form of FGFR3 mRNA in pituitary adenomas versus the lack of expression of the secretable form of this receptor in normal pituitary." However, none of the references teach the correlation between the gene expression profile of M64347 and effectiveness in treating a brain tumor selected from the group consisting of mellanoblastomas, glioblastomas, rhabdoid tumors, primitive neuroectodermal tumors, and pineoblastomas, or monitoring the efficacy of a treatment for any of the mentioned brain tumors. Therefore, there would be no motivation to combine the references as argued by the Examiner.

Further, even if the references were to be combined as suggested by the Examiner, the combination of references would not teach or suggest the inventions of claims 31 and 32. Rather, the combination of the references would <u>at best</u> teach the use of M64347 to evaluate drug candidates for their effectiveness in treating a pituitary adenoma, or to monitor the efficacy of a pituitary adenoma treatment. Nothing in the cited references suggests or discloses the use of M64347 to evaluate drug or monitor the efficacy of a drug to treat the brain tumors of the claims. Moreover, even if the references were combined, there would be no reasonable

expectation of success. Accordingly, Applicants respectfully request that the Examiner withdraw the obviousness rejections.

Conclusion

In view of the above, each of the presently pending claims in this application is believed to be in immediate condition for allowance. Accordingly, the Examiner is respectfully requested to pass this application to issue.

Applicant believes no fee is due with this response. However, if a fee is due, please charge our Deposit Account No. 18-1945, under Order No. WIBL-P01-561 from which the undersigned is authorized to draw.

Dated: July 15, 2004

Respectfully submitted,

By _____

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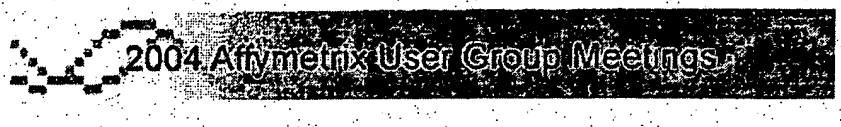

:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (m64347)
-> all probe sets (7129)

Full Record

Details for HUGENEFL:M64347_AT

Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	M64347_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	M64347
Sequence Type	Exemplar sequence
Representative Public ID	M64347 NCBI
Target Description	M64347, class A, 20 probes, 20 in M64347 3336-3720, Human novel growth facto receptor mRNA, 3' cds

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
	chr4: 1771773-1772182 (+) UCSC	93	p16.3

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_000142 NCBI	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261-1772237 (+) UCSC
	NM_022965 NCBI	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261-1772237 (+) UCSC

Public Domain and Genome References

Gene Title	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
Gene Symbol	FGFR3 HGNC
Chromosomal Location	4p16.3
UniGene ID	Hs.1420 NCBI (FULL LENGTH)
Ensembl	ENSG00000068078 Ensembl
LocusLink	2261 NCBI
	P22607 EMBL-EBI

SwissProt	Q96T34 EMBL-EBI Q96T35 EMBL-EBI Q96T36 EMBL-EBI Q9NRB6 EMBL-EBI
EC	2.7.1.112
OMIM	134934 NCBI
RefSeq Protein ID	NP_000133 NCBI NP_075254 NCBI

	RefSeq Transcript ID	RefSeq Title
RefSeq	NM_000142 NCBI	fibroblast growth factor receptor 3 isoform 1 precursor
	NM_022965 NCBI	fibroblast growth factor receptor 3 isoform 2 precursor

Functional Annotations

	ID	Title	Organism	Type
Ortholog	DROSGENOME1:143549_AT	breathless	Drosophila	Putative Ortholog
	RAE230A:1369373_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RAE230B:1384056_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RAE230B:1384829_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34B:RC_AA899336_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34C:RC_AI136304_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34C:RC_AI145424_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	MG-U74AV2:160919_R_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MG-U74AV2:162253_I_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOE430A:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOE430A:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MU11KSUBA:M81342_S_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430_2:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430_2:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430A_2:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430A_2:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
165	MAPKKK cascade	experimental evidence	QuickGO AmiGO
1501	skeletal development	predicted/computed	QuickGO AmiGO
7048	oncogenesis	experimental evidence	QuickGO AmiGO
7259	JAK-STAT cascade	experimental	QuickGO

			evidence	AmiGO
		8543 FGF receptor signaling pathway	experimental evidence	QuickGO AmiGO

GO Cellular Component (view graph)

	ID	Description	Evidence	Links
Gene Ontology	5887	integral to plasma membrane	experimental evidence	QuickGO AmiGO

GO Molecular Function (view graph)

	ID	Description	Evidence	Links
	5007	fibroblast growth factor receptor activity	experimental evidence	QuickGO AmiGO

	Method	ID	Description	E-Value
Protein Similarities	blast	13112048	fibroblast growth factor receptor 3 isoform 2 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]	0.0
	blast	13186255	fibroblast growth factor receptor 2 isoform 3 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase [Homo sapiens]	0.0
	blast	4503711	fibroblast growth factor receptor 3 isoform 1 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]	0.0
	blast	20452380		0.0

	Method	ID	Description	E-Value
Protein Families	Hanks	FGFR-3	FGR3_HUMAN (FGFR-3) KINASES:5.6.3 | PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3	1.0E-166
	ec	ZA70_HUMAN	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).	7.38E-99
	Hanks	FGFR-3	FGR3_HUMAN (FGFR-3) KINASES:5.6.3 | PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3	1.0E-167
	ec	ZA70_HUMAN	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).	7.38E-99

Database	ID	Description	E-Value
scop	d1gjoa_	d1gjoa_ SCOP:d.144.1.2:| Fibroblast growth factor receptor 2	3.81E-81
scop	d1ev2e1	d1ev2e1 SCOP:b.1.1.4:| Fibroblast growth factor receptor, FGFR	4.95E-21
scop	d1gjoa_	d1gjoa_ SCOP:d.144.1.2:| Fibroblast growth factor receptor 2	3.81E-81

Protein Domains

scop	d1ev2e1	d1ev2e1 SCOP:b.1.1.4:| Fibroblast growth factor receptor, FGFR	4.25E-21
pfam	ig	Immunoglobulin domain	1.6E-5
pfam	ig	Immunoglobulin domain	3.2E-8
pfam	pkinase	Protein kinase domain	2.3E-92
pfam	ig	Immunoglobulin domain	1.6E-5
pfam	ig	Immunoglobulin domain	3.2E-8
pfam	pkinase	Protein kinase domain	2.3E-92
pfam	ig	Immunoglobulin domain	7.3E-8
InterPro	IPR000719 EMBL-EBI	Protein kinase	
InterPro	IPR007110 EMBL-EBI	Immunoglobulin-like	
InterPro	IPR001245 EMBL-EBI	Tyrosine protein kinase	
InterPro	IPR008266 EMBL-EBI	Tyrosine protein kinase, active site	
InterPro	IPR003598 EMBL-EBI	Immunoglobulin C-2 type	

Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000133	2	0.11005

Sequence

Target Sequence

>HUGENEFL:M64347_AT
gacttcaaagcaagctggtattttcatacaaattcttctaattgctgtgtgtcccaggca
gggagacggtttccagggaggggccggccctgtgtgcaggttccgatgttattagatgtt
acaagtttatatatatctatatatataatttattgagttttacaagatgtatttgttgt
agacttaacacttcttacgcaatgcttctagagttttatagcctggactgctacctttca
aagcttggagggaagccgtgaattcagttggttcgttctgtactgttactgggccctgag
tctgggcagctgtcccttgcttgcctgcagggccatggctcagggtggtctcttcttggg
gcccagtgcatggtggccagaggtgtcacccaaaccggcaggtgcgatt

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GACTTCAAAGCAAGCTGGTATTTTC	359	161	3348	Antisense
CATACAAATTCTTCTAATTGCTGTG	360	161	3372	Antisense
AATTCTTCTAATTGCTGTGTGTCCC	361	161	3378	Antisense
TGCTGTGTGTCCCAGGCAGGGAGAC	362	161	3390	Antisense
TGTGTGCAGGTTCCGATGTTATTAG	363	161	3438	Antisense
TCTTACGCAATGCTTCTAGAGTTTT	364	161	3540	Antisense
GCAATGCTTCTAGAGTTTTATAGCC	365	161	3546	Antisense
GAGTTTTATAGCCTGGACTGCTACC	366	161	3558	Antisense
TGCTACCTTTCAAAGCTTGGAGGGA	367	161	3576	Antisense
AAGCTTGGAGGGAAGCCGTGAATTC	368	161	3588	Antisense
TGAATTCAGTTGGTTCGTTCTGTAC	369	161	3606	Antisense
GTTCGTTCTGTACTGTTACTGGGCC	370	161	3618	Antisense
CTGGGCCCTGAGTCTGGGCAGCTGT	371	161	3636	Antisense
CCTGAGTCTGGGCAGCTGTCCCTTG	372	161	3642	Antisense
TCTGGGCAGCTGTCCCTTGCTTGCC	373	161	3648	Antisense
TCCCTTGCTTGCCTGCAGGGCCATG	374	161	3660	Antisense

GCTTGCCTGCAGGGCCATGGCTCAG	375	161	3666	Antisense
CTTGGGGCCCAGTGCATGGTGGCCA	376	161	3702	Antisense
GTGGCCAGAGGTGTCACCCAAACCG	377	161	3720	Antisense
GTCACCCAAACCGGCAGGTGCGATT	378	161	3732	Antisense

Sequence Revision History

NCBI Home

Site Map
brief and complete versions

About NCBI
general and contact information

GenBank
submit your sequence, general information

Molecular Databases
nucleotides, proteins, structures and taxonomy

Literature Databases
PubMed, PubRef, OMIM, Citation Matcher

Genomes and Maps
maps, the human genome and model organisms

Tools
for data mining and analysis

Research at NCBI
people and projects

Software Engineering
Tools, R&D and databases

Education
teaching resources and on-line tutorials

FTP site

The Sequence Revision History tool allows you to see the various gi numbers, version numbers, and update dates for sequences that appeared in a specific GenBank record.

E.g., search for U46667 in the tool to see the old and current identifiers of the nucleotide sequence in that record.

Note that the original gi number for the nucleotide sequence, 2734632, does not have a corresponding version number. This is true because it was removed from the database (and replaced by 3172140) before the new accession.verion system was implemented in Feb. 1999. At that time, each sequence in the GenBank/EMBL/DDBJ database received a version number of 1, even if they had been updated in the past.

In addition, if a GenBank record contains an updated sequence, the Comment field will contain a cross-reference to the gi number of the earlier sequence. (E.g., see U46667 in Entrez.) If you follow the link for that earlier gi number, Entrez will display that version of the GenBank record. Similarly, the Comment field of the older version will have a warning that the sequence has been updated, and will contain a cross-reference to the newer version.

More details about sequence identification numbers (GI and accession.version).

Back to sample record.

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software

Revised October 1, 2003
Questions about NCBI resources to info@ncbi.nlm.nih.gov
Comments about site map to Renata Geer renata@ncbi.nlm.nih.gov

NCBI

Sequence Revision History

Revision history for U46667

GI	Version	Update Date	Status	I	II
3172140	1	Aug 7 1998 9:28 AM	Live	◉	○
3172140	1	Jun 2 1998 4:31 PM	Dead	○	◉
2734632	n/a	Jan 3 1998 12:12 AM	Dead	○	○
2734632	n/a	Jan 1 1998 12:30 AM	Dead	○	○

Accession U46667 was first seen at NCBI on Jan 1 1998 12:30 AM

Entrez

Search for Genes
LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Help|FAQ

Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

Check sequence revision history

How to create WWW links to Entrez

LinkOut

Cubby

Related resources

BLAST

Reference sequence project

LocusLink

Clusters of orthologous groups

Protein reviews on the web

:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY
1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (L17131)
-> (0)All Descriptions (L17131_rna1_at)
-> (0)All Descriptions (L17131_rna1_at)
-> (1)All Descriptions (m64347)
-> all probe sets (7129)
-> Genotyping Queries

Full Record

Details for HUGENEFL:L17131_RNA1_AT

Full Screen

NetAffx Links: Cluster Members; Consensus/Exemplar

GeneChip Array Information

Probe Set ID	L17131_rna1_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	L17131_rna1
Sequence Type	Exemplar sequence
Representative Public ID	L17131 NCBI
Target Description	L17131, class A, 20 probes, 20 in L17131mRNA#1 1646-2198, Human high mobility group protein (HMG-I(Y)) gene exons 1-8, complete cds

Sequence

Target Sequence

>HUGENEFL:L17131_RNA1_AT

ttgtccaggtgaggcccaagagccctgtggccgccacctgaggtgggctggggctgctcc
cctaaccctactttcgttccgccactcagccatttccccctcctcagatggggcaccaat
aacaaggagctcaccctgcccgctcccaaccccctcctgctcctccctgccccccaagg
ttctggttccatttttcctctgttcacaaactacctctggacagttgtgttgttttttgt
tcaatgttccattcttcgacatccgtcattgctgctgctaccagcgccaaatgttcatcc
tcattgcctcctgttctgcccacgatcccctcccccaagatactctttgtggggaagagg
ggctggggcatggcaggctgggtgaccgactaccccagtcccagggaaggtggggccctg
cccctaggatgctgcagcagagtgagcaaggggcccgaatcgaccataaagggtgtagg
ggccacctcctcccccctgttctgttggggaggggtagccatgatttgtcccagcctgggg
ctccctctctggtttcctatttgcagttacttgaata

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
TTGTCCAGGTGAGGCCCAAGAGCCC	294	101	1658	Antisense
AGGTGAGGCCCAAGAGCCCTGTGGC	295	101	1664	Antisense
ACCAATAACAAGGAGCTCACCCTGC	296	101	1772	Antisense
TTTTCCTCTGTTCACAAACTACCTC	297	101	1850	Antisense
CTACCTCTGGACAGTTGTGTTGTTT	298	101	1868	Antisense
TTCCATTCTTCGACATCCGTCATTG	299	101	1904	Antisense
TCTTCGACATCCGTCATTGCTGCTG	300	101	1910	Antisense

	GCTACCAGCGCCAAATGTTCATCCT	301	101	1934	Antisense
	TCATCCTCATTGCCTCCTGTTCTGC	302	101	1952	Antisense
	TCATTGCCTCCTGTTCTGCCCACGA	303	101	1958	Antisense
	AAGATACTCTTTGTGGGGAAGAGGG	304	101	1994	Antisense
	GCAGGCTGGGTGACCGACTACCCCA	305	101	2030	Antisense
	CCCCTAGGATGCTGCAGCAGAGTGA	306	101	2078	Antisense
Probe Info	AGCAAGGGGGCCCGAATCGACCATA	307	101	2102	Antisense
	CGAATCGACCATAAAGGGTGTAGGG	308	101	2114	Antisense
	GCCATGATTTGTCCCAGCCTGGGGC	309	101	2174	Antisense
	CTGGGGCTCCCTCTCTGGTTTCCTA	310	101	2192	Antisense
	CTCCCTCTCTGGTTTCCTATTTGCA	311	101	2198	Antisense
	CTCTGGTTTCCTATTTGCAGTTACT	312	101	2204	Antisense
	TTTCCTATTTGCAGTTACTTGAATA	313	101	2210	Antisense

:: GETTING STARTED
-> Wizard

:: QUERY Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query

Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY 1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY

Annotation Views
-> Expression
-> Genotyping

-> BLAST Status

-> New Folder

-> Expression Queries
-> (1)All Descriptions (X74801)
-> (1)All Descriptions (L17131)
-> (0)All Descriptions (L17131_rna1_at)
-> (0)All Descriptions (L17131_rna1_at)
-> (1)All Descriptions (m64347)

-> Genotyping Queries

Full Record

Details for HUGENEFL:X74801_AT

Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	X74801_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	X74801
Sequence Type	Exemplar sequence
Representative Public ID	X74801 NCBI
Target Description	X74801, class B, 20 probes, 12 in X74801cds 1282-1552: 8 in reverseSequence, 1636-1837, H.sapiens Cctg mRNA for chaperonin

Genomic Alignment of Target Sequence

Assembly	April 2003 (NCBI 33)		
	Position	% Identity	Cytoband
Alignment(s)	chr1: 153495555-153497649 (-) UCSC	100	q22

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_005998 NCBI	chaperonin containing TCP1, subunit 3 (gamma)	chr1:153495551-153524840 (-) UCSC

Public Domain and Genome References

Gene Title	chaperonin containing TCP1, subunit 3 (gamma)
Gene Symbol	CCT3 HGNC
Chromosomal Location	1q23
UniGene ID	Hs.1708 NCBI (FULL LENGTH)
Ensembl	ENSG00000163468 Ensembl
LocusLink	7203 NCBI
SwissProt	AAH06501 EMBL-EBI P49368 EMBL-EBI
OMIM	600114 NCBI
RefSeq Protein ID	NP_005989 NCBI

	RefSeq Transcript ID	RefSeq Title
RefSeq	NM_005998 NCBI	chaperonin containing TCP1, subunit 3 (gamma)

Functional Annotations

	ID	Title	Organism	Type
Ortholog	ATH1-121501:246830_AT	chaperonin, putative	Arabidopsis	Putative Ortholog
	ATGENOME1:18906_AT	chaperonin, putative	Arabidopsis	Putative Ortholog
	DROSGENOME1:153982_AT		Drosophila	Putative Ortholog
	MG-U74AV2:161238_F_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MG-U74AV2:98153_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MG-U74CV2:171548_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1416024_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1426067_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1448178_A_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1449645_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1451915_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1459987_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MU11KSUBA:C79428_RC_F_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MU11KSUBA:L20509_F_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1416024_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1426067_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1448178_A_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1449645_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1451915_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1459987_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1416024_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1426067_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1448178_A_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1449645_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1451915_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog

MOUSE430A_2:1459987_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog

Gene Ontology

GO Biological Process (view graph)

ID	Description	Evidence	Links
6457	protein folding	traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5829	cytosol	not recorded	QuickGO AmiGO
5856	cytoskeleton	traceable author statement	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
3754	chaperone activity	traceable author statement	QuickGO AmiGO
5524	ATP binding	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	33873532		0.0
blast	31542292	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring complex, polypeptide 5 [Homo sapiens]	0.0

Protein Domains

Database	ID	Description	E-Value
scop	d1a6da3	d1a6da3 SCOP:d.56.1.2:| Thermosome	4.08E-25
scop	d1gmla_	d1gmla_ SCOP:c.8.5.2:| Thermosome	1.01E-57
scop	d1a6da1	d1a6da1 SCOP:a.129.1.2:| Thermosome	4.81E-83
pfam	cpn60_TCP1	TCP-1/cpn60 chaperonin family	5.7E-210
InterPro	IPR002423 EMBL-EBI	Chaperonin Cpn60/TCP-1	
InterPro	IPR001844 EMBL-EBI	Chaperonin Cpn60	
InterPro	IPR002194 EMBL-EBI	Chaperonin TCP-1	
InterPro	IPR008950 EMBL-EBI	GroEL-like chaperone, ATPase	

Sequence

Target Sequence

>HUGENEFL:X74801_AT

atgactggtgtggaacaatggccatacagggctgttgcccaggccctagaggtcattcct
cgtaccctgatccagaactgtggggccagcaccatccgtctacttacctcccttcgggcc
aagcacacccaggagaactgtgagacctggggtgtaaatggtgagacgggtactttggtg
gacatgaaggaactgggcatatgggagccattggctgtgaagctgcagacttataagaca
gcagtggagacggcagttctgctactgcgaattgatgacatcgtttcaggccacaaaaag
aaaggcgatgaccagagccggcaaggcggggctcctgatgctggccaggagtgagtgcta
ggcaaggctacttcaatgcacagaaccagcagagtctccccttttcctgagccagagtgc
caggaacactgtggacgtctttgttcagaagggatcaggttgggggcagcccccagtcc
ctttctgtcccagctcagttttccaaaagacactgacatgtaattcttctctattgtaag
gtttccatttagtttgcttccgatgattaaatctaagtca

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness

Probe Info

ATGACTGGTGTGGAACAATGGCCAT	60	345	1294	Antisense
GAACAATGGCCATACAGGGCTGTTG	61	345	1306	Antisense
CTGATCCAGAACTGTGGGGCCAGCA	62	345	1360	Antisense
CAGAACTGTGGGGCCAGCACCATCC	63	345	1366	Antisense
TGTGGGGCCAGCACCATCCGTCTAC	64	345	1372	Antisense
CTGGGCATATGGGAGCCATTGGCTG	65	345	1486	Antisense
ATATGGGAGCCATTGGCTGTGAAGC	66	345	1492	Antisense
GAGCCATTGGCTGTGAAGCTGCAGA	67	345	1498	Antisense
TTGGCTGTGAAGCTGCAGACTTATA	68	345	1504	Antisense
GAGACGGCAGTTCTGCTACTGCGAA	69	345	1540	Antisense
GCAGTTCTGCTACTGCGAATTGATG	70	345	1546	Antisense
ATTGATGACATCGTTTCAGGCCACA	71	345	1564	Antisense
GTGCTAGGCAAGGCTACTTCAATGC	72	345	1648	Antisense
GGCAAGGCTACTTCAATGCACAGAA	73	345	1654	Antisense
GCTACTTCAATGCACAGAACCAGCA	74	345	1660	Antisense
CACAGAACCAGCAGAGTCTCCCCTT	75	345	1672	Antisense
GAGCCAGAGTGCCAGGAACACTGTG	76	345	1702	Antisense
CACTGACATGTAATTCTTCTCTATT	77	345	1804	Antisense
TAGTTTGCTTCCGATGATTAAATCT	78	345	1843	Antisense
GCTTCCGATGATTAAATCTAAGTCA	79	345	1849	Antisense

:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY
1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (U15008_at)
-> (1)All Descriptions (HG3523)
-> all probe sets (7129)
-> (1)All Descriptions (X74801)
-> (1)All Descriptions (L17131)
-> Genotyping Queries

Full Record

Details for HUGENEFL:U15008_AT

Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	U15008_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	U15008
Sequence Type	Exemplar sequence
Representative Public ID	U15008 NCBI
Target Description	U15008, class A, 20 probes, 20 in U15008 25-433, Human SnRNP core protein Sm D2 mRNA, complete cds

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

Alignment(s)	**Position**	**% Identity**	**Cytoband**
	chr19: 50882580-50883664 (-) UCSC	98	q13.32

Overlapping Transcripts	**Representative Transcript**	**UniGene Description**	**Position**
	NM_004597 NCBI	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	chr19:50882558-50887282 (-) UCSC
	NM_177542 NCBI	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	chr19:50882558-50887282 (-) UCSC

Public Domain and Genome References

Gene Title	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa
Gene Symbol	SNRPD2 HGNC
Chromosomal Location	19q13.2
UniGene ID	Hs.424327 NCBI (FULL LENGTH)
Ensembl	ENSG00000125743 Ensembl
LocusLink	6633 NCBI
SwissProt	P43330 EMBL-EBI
OMIM	601061 NCBI

RefSeq Protein ID	NP_004588 NCBI	
	NP_808210 NCBI	
RefSeq	RefSeq Transcript ID	RefSeq Title
	NM_004597 NCBI	small nuclear ribonucleoprotein polypeptide D2
	NM_177542 NCBI	small nuclear ribonucleoprotein polypeptide D2

Functional Annotations

	ID	Title	Organism	Type
Ortholog	ATH1-121501:266482_AT	small nuclear ribonucleo protein D2 -related	Arabidopsis	Putative Ortholog
	C. ELEGANS:172931_X_AT	small nuclear ribonucleoprotein D2 like	Celegans	Putative Ortholog
	DROSGENOME1:153483_AT		Drosophila	Putative Ortholog
	MG-U74AV2:95049_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MOE430A:1452680_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MU11KSUBA:AA271024_S_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MOUSE430_2:1452680_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MOUSE430A_2:1452680_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog

Gene Ontology

GO Biological Process (view graph)

ID	Description	Evidence	Links
245	spliceosome assembly	traceable author statement	QuickGO AmiGO
6371	mRNA splicing	traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5681	spliceosome complex	traceable author statement	QuickGO AmiGO
5732	small nucleolar ribonucleoprotein complex	inferred from electronic annotation	QuickGO AmiGO
30532	small nuclear ribonucleoprotein complex	traceable author statement	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
8248	pre-mRNA splicing factor activity	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	4759158	small nuclear ribonucleoprotein polypeptide D2; snRNP core protein D2 [Homo sapiens]	1.0E-62
blast	26337731		3.0E-62
blast	4759158	small nuclear ribonucleoprotein polypeptide D2; snRNP core protein D2 [Homo sapiens]	1.0E-62
blast	26337731		3.0E-62

Database	ID	Description	E-Value
scop	d1b34b_	d1b34b_ SCOP:b.38.1.1:| D2 core SNRNP	1.85E-

			protein	28
	scop	d1b34b_	d1b34b_ SCOP:b.38.1.1:| D2 core SNRNP protein	1.85E-28
Protein Domains	pfam	LSM	LSM domain	1.1E-16
	pfam	LSM	LSM domain	1.1E-16
	InterPro	IPR001163 EMBL-EBI	Small nuclear ribonucleoprotein (Sm protein)	

Sequence

Target Sequence

```
>HUGENEFL:U15008_AT
accatcatgagcctcctcaacaagcccaagagtgagatgaccccagaggagctgcagaag
cgagaggaggaggaatttaacaccggtccactctctgtgctcacacagtcagtcaagaac
aatacccaagtgctcatcaactgccgcaacaataagaaactcctgggccgcgtgaaggcc
ttcgataggcactgcaacatggtgctggagaacgtgaaggagatgtggactgaggtaccc
aagagtggcaagggcaagaagaagtccaagccagtcaacaaagaccgctacatctccaag
atgttcctgcgcggggactcagtcatcgtggtcctgcggaacccgctcatcgccggcaag
taggggccgcctgtctgttgacagaactcactcctctgtcctatgaagaccgctgccatt
ggtgttgagaata
```

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
ACCATCATGAGCCTCCTCAACAAGC	99	211	37	Antisense
AGTGAGATGACCCCAGAGGAGCTGC	100	211	67	Antisense
AACACCGGTCCACTCTCTGTGCTCA	101	211	115	Antisense
GGTCCACTCTCTGTGCTCACACAGT	102	211	121	Antisense
CTCTCTGTGCTCACACAGTCAGTCA	103	211	127	Antisense
GTGCTCACACAGTCAGTCAAGAACA	104	211	133	Antisense
TCAGTCAAGAACAATACCCAAGTGC	105	211	145	Antisense
AATACCCAAGTGCTCATCAACTGCC	106	211	157	Antisense
CAAGTGCTCATCAACTGCCGCAACA	107	211	163	Antisense
CGCGTGAAGGCCTTCGATAGGCACT	108	211	205	Antisense
AAGGCCTTCGATAGGCACTGCAACA	109	211	211	Antisense
TTCGATAGGCACTGCAACATGGTGC	110	211	217	Antisense
GTACCCAAGAGTGGCAAGGGCAAGA	111	211	271	Antisense
TACATCTCCAAGATGTTCCTGCGCG	112	211	325	Antisense
TCAGTCATCGTGGTCCTGCGGAACC	113	211	355	Antisense
TAGGGGCCGCCTGTCTGTTGACAGA	114	211	397	Antisense
TGACAGAACTCACTCCTCTGTCCTA	115	211	415	Antisense
CTCCTCTGTCCTATGAAGACCGCTG	116	211	427	Antisense
TGTCCTATGAAGACCGCTGCCATTG	117	211	433	Antisense
ACCGCTGCCATTGGTGTTGAGAATA	118	211	445	Antisense

:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY
1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (AFFX-BioB-M_st)
-> (1)All Descriptions (HG613)
-> (2)All Descriptions (AFFX-BioDn-5)
-> (2)All Descriptions (AFFX-BioB-M)
-> (1)All Descriptions (M12625_at)
-> Genotyping Queries

Full Record

Details for HUGENEFL:AFFX-BIOB-M_ST

Full Screen

NetAffx Links Cluster Members
Consensus/Exemplar

GeneChip Array Information

Probe Set ID	AFFX-BioB-M_st
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	AFFX-BioB-M
Sequence Type	Control sequence
Representative Public ID	J04423 NCBI
Target Description	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

Sequence

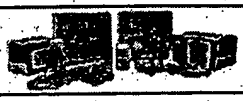
Target Sequence

```
>HUGENEFL:AFFX-BIOB-M_ST
gccggagttttacggcaatatcatcaccacacgcacttatcaggaacgcctcgatacgct
ggaaaaagtgcgcgatgccgggatcaaagtctgttctggcggcattgtgggcttaggcga
aacggtaaaagatcgcgccggattattgctgcaactggcaaacctgccgacgccgccgga
aagcgtgccaatcaacatgctggtgaaggtgaaaggcacgccgcttgccgataacgatga
tgtcgatgcctttgattt
```

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GATGATATTGCCGTAAAACTCCGGC	201	11	483	Sense
TGTGGTGATGATATTGCCGTAAAAC	202	11	489	Sense
TAAGTGCGTGTGGTGATGATATTGC	203	11	497	Sense
GTTCCTGATAAGTGCGTGTGGTGAT	204	11	505	Sense
ATCGAGGCGTTCCTGATAAGTGCGT	205	11	513	Sense
GCATCGCGCACTTTTTCCAGCGTAT	206	11	536	Sense
GATCCCGGCATCGCGCACTTTTTCC	207	11	543	Sense
GACTTTGATCCCGGCATCGCGCACT	208	11	549	Sense
CGCCAGAACAGACTTTGATCCCGGC	209	11	559	Sense
CCCACAATGCCGCCAGAACAGACTT	210	11	569	Sense

TGCAGCAATAATCCGGCGCGATCTT	211	11	611	Sense
TTGCCAGTTGCAGCAATAATCCGGC	212	11	619	Sense
CGGCAGGTTTGCCAGTTGCAGCAAT	213	11	627	Sense
ATGTTGATTGGCACGCTTTCCGGCG	214	11	656	Sense
CACCAGCATGTTGATTGGCACGCTT	215	11	663	Sense
TTCACCTTCACCAGCATGTTGATTG	216	11	671	Sense
AGCGGCGTGCCTTTCACCTTCACCA	217	11	683	Sense
CATCATCGTTATCGGCAAGCGGCGT	218	11	700	Sense
GCATCGACATCATCGTTATCGGCAA	219	11	707	Sense
AAATCAAAGGCATCGACATCATCGT	220	11	716	Sense



Full Record

Details for HUGENEFL:AFFX-BIODN-5_ST

Full Screen

NetAffx Links Cluster Members, Consensus/Exemplar

GeneChip Array Information

Probe Set ID	AFFX-BioDn-5_st
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	AFFX-BioDn-5
Sequence Type	Control sequence
Representative Public ID	J04423 NCBI
Target Description	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

Sequence

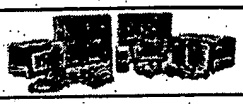
Target Sequence

>HUGENEFL:AFFX-BIODN-5_ST
gggaaaactgtcgccagttgtgcacttttacaagccgcaaaggcagcaggctaccggacg
gcaggttataaaccggtcgcctctggcagcgaaaagaccccggaaggtttacgcaatagc
gacgcgctggcgttacagcgcaacagcagcctgcagctggattacgcaacagtaaatcct
tacaccttcgcagaacccacttcgccgcacatcatcagcgcgcaagagggcagaccgata
gaatcattggtaatgagcgccggattacgcgcgcttg

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GTGCACAACTGGCGACAGTTTTCCC	281	11	49	Sense
GGCTTGTAAAAGTGCACAACTGGCG	282	11	60	Sense
GCTGCCTTTGCGGCTTGTAAAAGTG	283	11	71	Sense
GGTAGCCTGCTGCCTTTGCGGCTTG	284	11	79	Sense
CCGTCCGGTAGCCTGCTGCCTTTGC	285	11	85	Sense
CAGCGCGTCGCTATTGCGTAAACCT	286	11	153	Sense
GTAACGCCAGCGCGTCGCTATTGCG	287	11	160	Sense
TTGCGCTGTAACGCCAGCGCGTCGC	288	11	167	Sense
TGCTGTTGCGCTGTAACGCCAGCGC	289	11	172	Sense
TGCAGGCTGCTGTTGCGCTGTAACG	290	11	179	Sense

TCCAGCTGCAGGCTGCTGTTGCGCT	291	11	185	Sense
TGCGTAATCCAGCTGCAGGCTGCTG	292	11	192	Sense
TTACTGTTGCGTAATCCAGCTGCAG	293	11	199	Sense
CGGTCTGCCCTCTTGCGCGCTGATG	294	11	261	Sense
GATTCTATCGGTCTGCCCTCTTGCG	295	11	269	Sense
TACCAATGATTCTATCGGTCTGCCC	296	11	276	Sense
CTCATTACCAATGATTCTATCGGTC	297	11	281	Sense
TCCGGCGCTCATTACCAATGATTCT	298	11	288	Sense
CGCGTAATCCGGCGCTCATTACCAA	299	11	295	Sense
CAAGCGCGCGTAATCCGGCGCTCAT	300	11	301	Sense



:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY
1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (X15880_at)
-> (1)All Descriptions (HG4011-HT4804_s_at)
-> (1)All Descriptions (AFFX-BioDn-5_st)
-> (1)All Descriptions (AFFX-BioB-M_st)
-> (1)All Descriptions (HG613)
-> Genotyping Queries

Full Record

Details for HUGENEFL:X15880_AT

Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	X15880_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	X15880
Sequence Type	Exemplar sequence
Representative Public ID	X15880 NCBI
Target Description	X15880, class C, 20 probes, 20 in all_X15880 1690-2273, Human mRNA for collagen VI alpha-1 C-terminal globular domain

Genomic Alignment of Target Sequence

Assembly	April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
	chr21: 46280561-46281145 (+) UCSC	100	q22.3

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_001848 NCBI	collagen, type VI, alpha 1	chr21:46257869-46281164 (+) UCSC

Public Domain and Genome References

Gene Title	collagen, type VI, alpha 1
Gene Symbol	COL6A1 HGNC
Chromosomal Location	21q22.3
UniGene ID	Hs.415997 NCBI (FULL LENGTH)
Ensembl	ENSG00000142156 Ensembl
LocusLink	1291 NCBI
SwissProt	P12109 EMBL-EBI Q7Z645 EMBL-EBI Q8TBN2 EMBL-EBI Q9BSA8 EMBL-EBI
OMIM	120220 NCBI

RefSeq Protein ID NP_001839 NCBI

RefSeq

RefSeq Transcript ID	RefSeq Title
NM_001848 NCBI	collagen, type VI, alpha 1 precursor

Functional Annotations

Ortholog

ID	Title	Organism	Type
MG-U74AV2:162459_F_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
MG-U74AV2:95493_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
MOE430A:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
MU11KSUBB:X66405_S_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
MOUSE430_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
MOUSE430A_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog

Gene Ontology

GO Biological Process (view graph)

ID	Description	Evidence	Links
7155	cell adhesion	non-traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5578	extracellular matrix	inferred from electronic annotation	QuickGO AmiGO
5589	collagen type VI	non-traceable author statement	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
5194	cell adhesion molecule activity	inferred from electronic annotation	QuickGO AmiGO
5201	extracellular matrix structural constituent	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	15011913		0.0
blast	13878903		0.0

Protein Domains

Database	ID	Description	E-Value
scop	d1atza_	d1atza_ SCOP:c.62.1.1:| von Willebrand factor A3 domain	3.63E-37
pfam	vwa	von Willebrand factor type A domain	9.6E-24
pfam	vwa	von Willebrand factor type A domain	4.7E-32
pfam	vwa	von Willebrand factor type A domain	2.7E-35
pfam	Collagen	Collagen triple helix repeat (20 copies)	2.4E-11
pfam	Collagen	Collagen triple helix repeat (20 copies)	3.8E-14
pfam	Collagen	Collagen triple helix repeat (20 copies)	3.3E-10
pfam	Collagen	Collagen triple helix repeat (20 copies)	2.6E-11
InterPro	IPR008161 EMBL-EBI	Collagen helix repeat	
InterPro	IPR002035 EMBL-EBI	von Willebrand factor, type A	

InterPro IPR008160 Collagen triple helix repeat
EMBL-EBI

Sequence

Target Sequence

>HUGENEFL:X15880_AT
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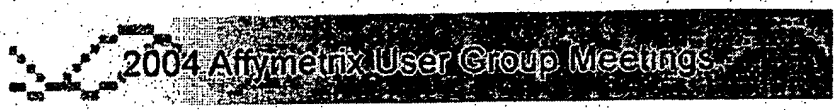
tgtgtttttttctgaaccatatccatgttgctgacttttccaa

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
AGCAAGACGCCTCTCGGGGCCTGTG	76	317	1702	Antisense
AAACTCAAAGCAAGCTCTTCTCCTC	77	317	1804	Antisense
AAAGCAAGCTCTTCTCCTCAGCTTG	78	317	1810	Antisense
TCTCCTCAGCTTGGGGCAGCCATTG	79	317	1822	Antisense
GCCATTGGCCTCTGTCTCGTTTTGG	80	317	1840	Antisense
GCAGACATAAATCTCGGCGACTCGG	81	317	1888	Antisense
GCCCCGTCTCCTGAGGGTCCTGCTG	82	317	1912	Antisense
TGGCCCTACAGCCCTGGAGGCCGCT	83	317	1954	Antisense
TCAGAGAGTACTCGCAGGGGCGCTG	84	317	2002	Antisense
AGTACTCGCAGGGGCGCTGGCTGCA	85	317	2008	Antisense
GGCGCTGGCTGCACTCAAGACCCTC	86	317	2020	Antisense
GGACATGAGAGCCCCTTGGTGCCAC	87	317	2104	Antisense
GAGAGCCCCTTGGTGCCACAGAGGG	88	317	2110	Antisense
CCCTTGGTGCCACAGAGGGCTGTGT	89	317	2116	Antisense
GTGCCACAGAGGGCTGTGTCTTACT	90	317	2122	Antisense
CAGAGGGCTGTGTCTTACTAGAAAC	91	317	2128	Antisense
CTCCTTCCTCAGAATAGTGATGTGT	92	317	2164	Antisense
TTTTTCTGAACCATATCCATGTTGC	93	317	2248	Antisense
TGAACCATATCCATGTTGCTGACTT	94	317	2254	Antisense
ATATCCATGTTGCTGACTTTTCCAA	95	317	2260	Antisense



:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY
1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (U23752_at)
-> (1)All Descriptions (HG1800-HT1823_at)
-> (1)All Descriptions (U15008_at)
-> (1)All Descriptions (HG3523)
-> all probe sets (7129)
-> Genotyping Queries

Full Record

Details for HUGENEFL:U23752_AT

Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	U23752_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	U23752
Sequence Type	Exemplar sequence
Representative Public ID	U23752 NCBI
Target Description	U23752, class A, 20 probes, 20 in U23752 1679-1919, Human SOX-11 mRNA, complete cds

Genomic Alignment of Target Sequence

Assembly: April 2003 (NCBI 33)

Alignment(s)

Position	% Identity	Cytoband
chr2: 5856192-5856457 (+) UCSC	99	p25.2

Overlapping Transcripts

Representative Transcript	UniGene Description	Position
NM_003108 NCBI	SRY (sex determining region Y)-box 11	chr2:5854537-5863255 (+) UCSC

Public Domain and Genome References

Gene Title	SRY (sex determining region Y)-box 11
Gene Symbol	SOX11 HGNC
Chromosomal Location	2p25
UniGene ID	Hs.432638 NCBI (FULL LENGTH)
Ensembl	ENSG00000176887 Ensembl
LocusLink	6664 NCBI
SwissProt	P35716 EMBL-EBI
OMIM	600898 NCBI
RefSeq Protein ID	NP_003099 NCBI

RefSeq

RefSeq Transcript ID	RefSeq Title
NM_003108 NCBI	SRY-box 11

Functional Annotations

Ortholog

ID	Title	Organism	Type
RAE230A:1387275_AT	SRY-box containing gene 11	Rat	Putative Ortholog
RG-U34A:AJ004858_AT	SRY-box containing gene 11	Rat	Putative Ortholog

Gene Ontology

GO Biological Process (view graph)

ID	Description	Evidence	Links
6355	regulation of transcription, DNA-dependent	inferred from electronic annotation	QuickGO AmiGO
7399	neurogenesis	traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5634	nucleus	inferred from electronic annotation	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
3677	DNA binding	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	4507161	SRY-box 11; SRY (sex-determining region Y)-box 11; SRY-related HMG-box gene 11; transcription factor SOX-11 [Homo sapiens]	0.0
blast	23831472		0.0

Protein Domains

Database	ID	Description	E-Value
scop	d1i11a_	d1i11a_ SCOP:a.21.1.1:| Sox-5	2.36E-19
pfam	HMG_box	HMG (high mobility group) box	1.1E-33
InterPro	IPR000910 EMBL-EBI	HMG1/2 (high mobility group) box	

Sequence

Target Sequence

```
>HUGENEFL:U23752_AT
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aaaaaatgtgtttttgtaattactatttctttttcctgaaattcgtgattgcaacaaagg
cagaggggcggcgcggcggaggggaggtaggacccgctccggaaggcgctgtttgaagc
ttgtcggtctttgaagtctggaagacgtctgcagaggacccttttggcagcacaactgtt
actctagggagttggtggagatatt
```

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
CTTCCTTTATCGTGTCTCAAGGTAG	503	219	1691	Antisense
TTATCGTGTCTCAAGGTAGTTGCAT	504	219	1697	Antisense
TCGTGTCTCAAGGTAGTTGCATACC	505	219	1700	Antisense
AAGGTAGTTGCATACCTAGTCTGGA	506	219	1709	Antisense
GTAGTTGCATACCTAGTCTGGAGTT	507	219	1712	Antisense

	GTTGCATACCTAGTCTGGAGTTGTG	508	219	1715	Antisense
	TACCTAGTCTGGAGTTGTGATTATT	509	219	1721	Antisense
	CTAGTCTGGAGTTGTGATTATTTTC	510	219	1724	Antisense
	TGTGATTATTTTCCCAAAAAATGTG	511	219	1736	Antisense
	TTTTCCTGAAATTCGTGATTGCAAC	512	219	1781	Antisense
	GCTCCGGAAGGCGCTGTTTGAAGCT	513	219	1847	Antisense
	GCTGTTTGAAGCTTGTCGGTCTTTG	514	219	1859	Antisense
Probe Info	TGAAGCTTGTCGGTCTTTGAAGTCT	515	219	1865	Antisense
	TTGTCGGTCTTTGAAGTCTGGAAGA	516	219	1871	Antisense
	TGGAAGACGTCTGCAGAGGACCCTT	517	219	1889	Antisense
	AAGACGTCTGCAGAGGACCCTTTTG	518	219	1892	Antisense
	GCAGAGGACCCTTTTGGCAGCACAA	519	219	1901	Antisense
	AGCACAACTGTTACTCTAGGGAGTT	520	219	1919	Antisense
	ACTGTTACTCTAGGGAGTTGGTGGA	521	219	1925	Antisense
	ACTCTAGGGAGTTGGTGGAGATATT	522	219	1931	Antisense

:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY
1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (M12625_at)
-> (1)All Descriptions (U23752_at)
-> (1)All Descriptions (HG1800-HT1823_at)
-> (1)All Descriptions (U15008_at)
-> (1)All Descriptions (HG3523)
-> Genotyping Queries

Full Record

Details for HUGENEFL:M12625_AT

Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	M12625_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	M12625
Sequence Type	Exemplar sequence
Representative Public ID	M12625 NCBI
Target Description	M12625, class B, 20 probes, 13 in M12625mRNA 893-1259: 7 in reverseSequence, 1599-1683, Human lecithin-cholesterol acyltransferase mRNA, complete cds, with 5' and 3' flanking DNA sequences

Genomic Alignment of Target Sequence

Assembly	April 2003 (NCBI 33)

Alignment(s)	**Position**	**% Identity**	**Cytoband**
	chr16: 67749925-67750484 (-) UCSC	100	q22.1

Overlapping Transcripts	**Representative Transcript**	**UniGene Description**	**Position**
	M12625 NCBI	lecithin-cholesterol acyltransferase	chr16:67749888-67754507 (-) UCSC

Public Domain and Genome References

Gene Title	lecithin-cholesterol acyltransferase
Gene Symbol	LCAT HGNC
Chromosomal Location	16q22.1
UniGene ID	Hs.387239 NCBI (FULL LENGTH)
Ensembl	ENSG00000103080 Ensembl
LocusLink	3931 NCBI
SwissProt	AAP88750 EMBL-EBI P04180 EMBL-EBI
EC	2.3.1.43
OMIM	606967 NCBI

RefSeq Protein ID NP_000220 NCBI

RefSeq

RefSeq Transcript ID	RefSeq Title
NM_000229 NCBI	lecithin-cholesterol acyltransferase precursor

Functional Annotations

Ortholog

ID	Title	Organism	Type
MG-U74AV2:103023_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MG-U74AV2:161759_R_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MOE430A:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MU11KSUBA:J05154_S_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
RAE230A:1367887_AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
RG-U34A:X54096_AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
MOUSE430_2:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MOUSE430A_2:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog

Gene Ontology

GO Biological Process (view graph)

ID	Description	Evidence	Links
6629	lipid metabolism	inferred from electronic annotation	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5576	extracellular	not recorded	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
4607	phosphatidylcholine-sterol O-acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
8415	acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
16740	transferase activity	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	32879837		0.0
blast	4557892	lecithin-cholesterol acyltransferase precursor [Homo sapiens]	0.0

Protein Families

Method	ID	Description	E-Value
ec	LCAT_HUMAN	LCAT_HUMAN EC:2.3.1.43:PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).	1.85E-171

Database	ID	Description	E-Value

Protein Domains

scop	d1tca__	d1tca__ SCOP:c.69.1.17:| Triacylglycerol lipase	5.3E-8
pfam	LACT	Lecithin:cholesterol acyltransferase	1.7E-182
InterPro	IPR003386 EMBL-EBI	Lecithin:cholesterol acyltransferase	
InterPro	IPR008262 EMBL-EBI	Lipase, active site	

Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000220	2	0.05945

Sequence

Target Sequence

>HUGENEFL:M12625_AT
cttcaactacacaggccgtgacttccaacgcttctttgcagacctgcactttgaggaagg
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agtatactgtctttacggcgtgggcctgcccacgccccgcacctacatctacgaccacgg
cttcccctacacggaccctgtgggtgtgctctatgaggatggtgatgacacggtggcgac
ccgcagcaccgagctctgtggcctgtggcagggccgccagccacagcctgtgcacctgct
gcccctgcacgggatacagcatctcaacatggtcttcagcaacctgaccctggagcacat
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ttcaggttgaagggaggcactagagtcccacactaggtttcactcctcaccagccacagg
ctcagtgctgtgtgcagtg

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
CTTCAACTACACAGGCCGTGACTTC	152	127	1161	Antisense
CTACACAGGCCGTGACTTCCAACGC	153	127	1167	Antisense
CCAACGCTTCTTTGCAGACCTGCAC	154	127	1185	Antisense
CCTGCACTTTGAGGAAGGCTGGTAC	155	127	1203	Antisense
CATGTGGCTGCAGTCACGTGACCTC	156	127	1227	Antisense
GCTGCAGTCACGTGACCTCCTGGCA	157	127	1233	Antisense
CCTGGCAGGACTCCCAGCACCTGGT	158	127	1251	Antisense
GGACCCTGTGGGTGTGCTCTATGAG	159	127	1353	Antisense
TGTGCTCTATGAGGATGGTGATGAC	160	127	1365	Antisense
GGCGACCCGCAGCACCGAGCTCTGT	161	127	1395	Antisense
CCTGACCCTGGAGCACATCAATGCC	162	127	1503	Antisense
GCACATCAATGCCATCCTGCTGGGT	163	127	1515	Antisense
CATCCTGCTGGGTGCCTACCGCCAG	164	127	1527	Antisense
CTTTGCTACCGTAAGCCCTGATGGC	165	127	1611	Antisense
TACCGTAAGCCCTGATGGCTATGTT	166	127	1617	Antisense
AAGCCCTGATGGCTATGTTTCAGGT	167	127	1623	Antisense
CTATGTTTCAGGTTGAAGGGAGGCA	168	127	1635	Antisense
GGAGGCACTAGAGTCCCACACTAGG	169	127	1653	Antisense
GTCCCACACTAGGTTTCACTCCTCA	170	127	1665	Antisense
CACAGGCTCAGTGCTGTGTGCAGTG	171	127	1695	Antisense